

GENETICS

FlyBase:ElP74EF

 #cross-references FlyBase:FBgn0005567

CLASSIFICATION

 #superfamily ets DNA-binding domain homology

KEYWORDS

 alternative splicing; DNA binding; transcription regulation

FEATURE

 788-869

 #domain ets DNA-binding domain homology #label ETS

SUMMARY

 #length 883 #molecular-weight 94819 #checksum 1974

Query Match 13.7%; Score 372; DB 2; Length 883;

 Best Local Similarity 34.9%; Pred. No. 9. 0.06e-49;

 Matches 59; Conservative 46; Mismatches 57; Indels 7; Gaps 7;

Db 707 SSSSSAAAMLSASAAAATAAAGGSSVSIOPATSSY-S-YVLS-YMLELGFQQR 763

OY 186 PGAPSPOSSDVSTARTATPOSSHASDGGSDVDLDIJKESKVFPDRDPTDYKKGEPKHGR 245

Db 764 KAKKKRK-PK-L-E-MGKRRSREGGSTYLWFLKLQLDRECYPRPRIWTNREKQVFKL 819

OY 246 KRGPRPKLWVDCLEGKKSRRHAPGTHWIFRDILHPELNEGLMKWENRHEGVKEF 305

Db 820 VDSKAVSLWGMHKNKPDMDNEYTMGRALRYVYORGILAKVQDQLYHF 868

OY 306 LASEAQHOLWGMOKKNSMTYEKLSRAMYVYKRETEILERVDOGRRLYKF 354

RESULT 6

ENTRY B53225 #type complete

TITLE ecdysone-induced protein E74A - fruit fly (Drosophila virilis)

ORGANISM #formal_name Drosophila virilis

DATE 21-May-1994 #sequence_revision 12-May-1994 #text_change

ACCESSIONS

REFERENCE A53225

 authors Jones, C.W.; Dalton, M.W.; Townley, L.H.

 title Genetics (1991) 17:1535-43

#cross-references MURID:91200627

accession B53225

 #status Preliminary; not compared with conceptual translation

 #molecule_type mRNA

 #residues 1-873 #label JON

#cross-references GB:X59493

GENETICS

gene

 #cross-references FlyBase:FBgn0013076

STRUCTURE

 #superfamily ets DNA-binding domain homology

SUMMARY

 #length 873 #molecular-weight 94630 #checksum 6269

Query Match 13.6%; Score 369; DB 2; Length 873;

 Best Local Similarity 47.3%; Pred. No. 3..8e-48;

 Matches 43; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

Db 768 KRASRREGSTTYIWEFLIKLQDREYCPRFIKWNREKGVKFLWDSKAVSLWGMHKNKPD 827

OY 264 KSKHARGHTRGLMEWFIRDILHPELNELNEGLMKVNENRHEGVFKLRSSEAQAOLWGMOKKNS 323

Db 828 MNVETMGRALRYVYORGILAKVQDQLYHF 858

OY 324 MTYEKLSRAMYYKRETEILERVDOGRRLYKF 354

RESULT 7

ENTRY G02318 #type complete

TITLE Ets transcription factor - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 17-Jul-1998

ACCESSIONS

REFERENCE H01044

 #authors Libermann, T.

 #submission submitted to the EMBL Data Library, December 1995

G02318

CLASSIFICATION

 #status preliminary; translated from GB/EMBL/DDBJ

KEYWORDS

 #molecule_type mRNA

 #residues 1-881 #label LIB

GENETICS

gene

 #cross-references EMBL:043188; NID:91420888; PID:91420889

CLASSIFICATION

 #superfamily ets DNA-binding domain homology

FEATURE

 198-278

 #length #domain ets DNA-binding domain homology #label ETS

SUMMARY

 #length 581 #molecular-weight 62711 #checksum 2023

Query Match 13.0%; Score 353; DB 2; Length 581;

 Best Local Similarity 44.6%; Pred. No. 5. 33e-45;

 Matches 41; Conservative 21; Mismatches 29; Indels 1; Gaps 1;

Db 186 KRPREGKNTTYLWFLDLIQDKWTCPRVTKTREKGIFKLVPSKAVSKLWGKHKNP 245

OY 264 KRSKHA-PRGTHLWEFIRDILHPELNELNEGLMKWENRHEGVFKFLRSEAVAOLWGMOKKNS 322

Db 246 DMVETMGRALRYVYORGILAKVQDQLYHF 277

OY 323 NNTYEKLSRAMYVYKRETEILERVDOGRRLYKF 354

RESULT 8

ENTRY A43361 #type complete

TITLE Ets-related transcription factor Elf-1 - human

ORGANISM #formal_name Homo Sapiens #common_name man

DATE 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change

ACCESSIONS

REFERENCE A43361; A42122

 authors Leiden, J.M.; Wang, C.Y.; Petryniak, B.; Markovitz, D.M.; Nabel, G.J.; Thompson, C.B.

 journal J. Virol. (1992) 66:5890-5897

 #title A novel Ets-related transcription factor, Elf-1, binds to human immunodeficiency virus type 2 regulatory elements that are required for inducible trans activation in T cells.

accession A43361

 #molecule_type mRNA

 #residues 1-619 #label LEI

 #cross-references GB:M62882

REFERENCE A42122

 authors Thompson, C.B.; Wang, C.Y.; Ho, I.C.; Bohjanen, P.R.; Petryniak, B.; June, C.H.; Miesfeldt, S.; Zhang, L.; Nabel, G.J.; Karpiński, B.; Leiden, J.M.

 journal Mol. Cell. Biol. (1992) 12:1043-1053

 #title cis-acting sequences required for inducible interleukin-2 enhancer function bind a novel Ets-related protein, Elf-1.

#cross-references MURID:9128836

accession A42122

 #status Preliminary; not compared with conceptual translation

 #molecule_type mRNA

 #residues 204-282, 'G', 284-289 #label THO

 #experimental_source T-cells

 #note sequence extracted from NCBI backbone (NCBIP:882880)

GENETICS

gene

 #cross-references GDB:BLF1

STRUCTURE

 #map_position 1p36.1p35

CLASSIFICATION

 #superfamily ets DNA-binding domain homology

KEYWORDS

 DNA binding; transcription regulation

FEATURE

 210-290

SUMMARY

 #length 619 #molecular-weight 67455 #checksum 5026

ACCESSIONS I48755 21-Aug-1998
 REFERENCE A53837 #journal Genovane, A.; Pintzas, A.; Maira, S.M.; Sobieszczuk, P.; Waslyk, B.
 #title Genes Dev. (1994) 8:1502-1513
 #cross-references MUID:93047310 factor that is activated by Ras.
 accession 148755 #status preliminary; translated from GB/EMBL/DDJB
 #residues 1-430 #label RES
 #cross-references EMBL:236885; NID:9535127; PID:9535128
 CLASSIFICATION #superfamily elk-1 transforming protein; ets DNA-binding domain homology
 FEATURE 7-85 #domain ets DNA-binding domain homology #label ETS
 SUMMARY #length 430 #molecular-weight 46867 #checksum 6382

Query Match Best Local Similarity 12.5%; Score 339; DB 2; Length 430;
 matches 38; Conservative; Pred. No. 3.05e-42; Gaps 2;
 Indels 2;

OY 7 LWFPLQLQEQPQ-NKHMICWTS-NGNEGLKQAEVARLWGRKRNKNMNDKLSRALR 64
 Db 65 YYYVKNIKVNGQKFVYKF 84
 OY 335 YYKKREILERVGRRLVYKF 354

RESULT 13 Query Match Best Local Similarity 12.5%; Score 339; DB 2; Length 430;
 ENTRY A42093 #type complete serum response factor accessory protein-1 form b (SAP-1b)
 TITLE -
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
 ACCESSIONS 21-Aug-1998
 REFERENCE A42093; S28816
 #authors Dalton, S.; Treisman, R.
 #journal Cell (1992) 68:597-612
 #title Characterization of SAP-1, a protein recruited by serum response factor to the c-fos serum response element.
 #cross-references MUID:92154673
 accession A42093 #status preliminary
 #molecule_type mRNA
 #residues 1-405 #label DAL
 #cross-references GB:M85164; NID:9338034; PID:9338035
 #experimental_source HeLa cells
 #note sequence extracted from NCBI backbone (NCBIN:82525, NCBIP:82527)
 CLASSIFICATION #superfamily elk-1 transforming protein; ets DNA-binding domain homology
 KEYWORDS DNA binding
 FEATURE 7-85 #domain ets DNA-binding domain homology #label ETS
 SUMMARY #length 405 #molecular-weight 44674 #checksum 4750

Query Match Best Local Similarity 47.5%; Score 339; DB 2; Length 430;
 matches 38; Conservative; Pred. No. 3.05e-42; Gaps 2;
 Indels 2;

OY 7 LWFPLQLQEQPQ-NKHMICWTS-NGNEGLKQAEVARLWGRKRNKNMNDKLSRALR 64
 Db 65 YYYVKNIKVNGQKFVYKF 84
 OY 335 YYKKREILERVGRRLVYKF 354

RESULT 15 Query Match Best Local Similarity 46.3%; Score 334; DB 2; Length 453;
 ENTRY A41354 #type complete transforming protein elk-1 - human
 TITLE -
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
 05-Sep-1997
 ACCESSIONS A41354; S24721
 REFERENCE A41354
 #authors Rao, V.N.; Huebler, K.; Isobe, M.; ar-Rushdi, A.; Croce, C.M.; Reddy, E.S.P.
 #journal Science (1989) 244:66-70
 #title elk, tissue-specific ets-related genes on chromosomes X and 14 near translocation breakpoints.
 #cross-references MUID:89203250
 accession A41354
 #molecule_type mRNA
 #residues 1-428 #label RAO
 #cross-references GB:M25209; NID:9538208; PID:9538209
 REFERENCE S54721
 #authors Gille, H.; Kortenjann, M.; Thomas, O.; Moomaw, C.; Slaughter, C.; Cobb, M.H.; Shaw, P.E.
 #journal EMBO J (1995) 14:951-962
 #title ERK phosphorylation potentiates Elk-1-mediated ternary complex formation and transactivation.
 #cross-references MUID:95196758
 accession S54721
 #status preliminary
 #molecule_type protein
 #residues 318-348, 'XX', 31:335-364, 380-388, 'X', 390-392, 'X', 394-400, 'XX', 403-405, 'X', 407-408 #label GIL

Query Match Best Local Similarity 46.3%; Score 334; DB 2; Length 405;
 matches 37; Conservative; Pred. No. 2.92e-41; Gaps 2;
 Indels 2;

OY 7 LWFLQLQEQPQ-NKHMICWTS-NGNEGLKQAEVARLWGRKRNKNMNDKLSRALR 64
 Db 65 YYYVKNIKVNGQKFVYKF 84
 OY 335 YYKKREILERVGRRLVYKF 354